

SEQUENCE LISTING

<110> Ono Pharmaceutical Co., Ltd.

<120> Novel Polypeptides, cDNA encoding the same, and use of them

<130> Q61459

<140> 09/700,397

<141> 2000-11-14

<150> JP 10-131815

<151> 1998-05-14

<150> PCT/JP99/02485

<151> 1999-05-13

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<170> PatentIn version 3.0

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Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser	
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Lys Trp Cys Leu Asp Pro Arg Val Val Leu Leu Ser Asn Thr Gln Thr
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Gln Tyr Ser Ile Glu Ile Gln Asn Val Asp Val Tyr Asp Glu Gly Pro
 70 75 80

Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser Arg Val
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His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser Asp
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Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr
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Gly Arg Pro Glu Pro Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala
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Ala Pro Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr
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 65 70 75 80

Pro Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser Arg
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Val His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser
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Lys Arg Tyr Leu Thr Ile Gly Leu Ser Ser Val Lys Arg Lys Lys Gly	
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Arg Lys Arg Tyr Leu Thr Ile Gly Leu Ser Ser Val Lys Arg Lys Lys
 100 105 110

Gly Asn Tyr Leu Leu Glu Thr Ile Lys Ser Ile Phe Glu Gln Ser Ser

115	120	125
Tyr Glu Glu Leu Lys Glu Ile Ser Val Val Ile His Leu Ala Asp Phe 130 135 140		
Asn Ser Ser Trp Arg Asp Ala Met Val Gln Asp Ile Thr Gln Lys Phe 145 150 155 160		
Ala His His Ile Ile Ala Gly Arg Leu Met Val Ile His Ala Pro Glu 165 170 175		
Glu Tyr Tyr Pro Ile Leu Asp Gly Leu Lys Arg Asn Tyr Asn Asp Pro 180 185 190		
Glu Asp Arg Val Lys Phe Arg Ser Lys Gln Asn Val Asp Tyr Thr Phe 195 200 205		
Leu Leu Asn Phe Cys Ala Asn Thr Ser Asp Tyr Tyr Val Met Leu Glu 210 215 220		
Asp Asp Val Arg Cys Ser Lys Asn Phe Leu Thr Ala Ile Lys Lys Val 225 230 235 240		
Ile Ala Ser Leu Glu Gly Thr Tyr Trp Val Thr Leu Glu Phe Ser Lys 245 250 255		
Leu Gly Tyr Ile Gly Lys Leu Tyr His Ser His Asp Leu Pro Arg Leu 260 265 270		
Ala His Phe Leu Leu Met Phe Tyr Gln Glu Met Pro Cys Asp Trp Leu 275 280 285		
Leu Thr His Phe Arg Gly Leu Leu Ala Gln Lys Asn Val Ile Arg Phe 290 295 300		
Lys Pro Ser Leu Phe Gln His Met Gly Tyr Tyr Ser Ser Tyr Lys Gly 305 310 315 320		
Thr Glu Asn Lys Leu Lys Asp Asp Asp Phe Glu Glu Glu Ser Phe Asp 325 330 335		

Ile Pro Asp Asn Pro Pro Ala Ser Leu Tyr Thr Asn Met Asn Val Phe
 340 345 350

Glu Asn Tyr Glu Ala Ser Lys Ala Tyr Ser Ser Val Asp Glu Tyr Phe
 355 360 365

Trp Gly Lys Pro Pro Ser Thr Gly Asp Val Phe Val Ile Val Phe Glu
 370 375 380

Asn Pro Ile Ile Ile Lys Lys Ile Lys Val Asn Thr Gly Thr Glu Asp
 385 390 395 400

Arg Gln Asn Asp Ile Leu His His Gly Ala Leu Asp Val Gly Glu Asn
 405 410 415

Val Met Pro Ser Lys Gln Arg Gly Gln Cys Ser Thr Tyr Leu Arg Leu
 420 425 430

Gly Glu Phe Lys Asn Gly Asn Phe Glu Met Ser Gly Val Asn Gln Lys
 435 440 445

Ile Pro Phe Asp Ile His Cys Met Arg Ile Tyr Val Thr Lys Thr Gln
 450 455 460

Lys Glu Trp Leu Ile Ile Arg Ser Ile Ser Ile Trp Thr Ser
 465 470 475

<210> 9
 <211> 1005
 <212> DNA
 <213> Homo sapiens

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 agcactacgc ggccgccttc cacgcccag ggcacgcgc tggcctacgg cagcctcctg 120
 ctcatggcgc tgctgcccac cttcttcggc gccctgcgct ccgtacgctg cgcccgcggc 180
 aagaatgctt cagacatgcc tgaaacaatc accagccggg atgccgcccg cttccccatc 240
 atcgccagct gcacactctt ggggctctac ctctttttca aaatattctc ccaggagtac 300
 atcaacctcc tgctgtccat gtatttcttc gtgctgggaa tcctggccct gtcccacacc 360
 atcagcccct tcatgaataa gttttttcca gccagctttc caaatcgaca gtaccagctg 420

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ctcttcacac aggggttctgg ggaaaacaag gaagagatca tcaattatga atttgacacc 480
aaggacctgg tgtgcctggg cctgagcagc atcgttggcg tctggtacct gctgaggaag 540
gtatttggca ccaatgtgat ggtgacagtg gccaaagtct tcgaggcacc aataaaattg 600
gtgtttcccc aggatctgct ggagaaaggc ctcgaagcaa acaactttgc catgctggga 660
cttgagatg tcgtcattcc agggatcttc attgccttgc tgctgcgctt tgacatcagc 720
ttgaagaaga atacccacac ctacttctac accagctttg cagcctacat ctcggcctg 780
ggccttacca tcttcacat gcacatcttc aagcatgctc agcctgcctt cctatacctg 840
gtccccgcct gcacgggttt tctgtctctg gtggcgctgg ccaagggaga agtgacagag 900
atgttcagtt atgaggagtc aaatcctaag gatccagcgg cagtgcaga atccaaagag 960
ggaacagagg catcagcatc gaaggggctg gagaagaaag agaaa 1005

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<210> 10
<211> 1486
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<223> Clone OA004b derived from T98G cell

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<220>
<221> CDS
<222> (117)..(1121)

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ctgcgtccct gctgcagcaa ccggagctgg agtcggatcc cgaacgcacc ctcgcc atg 119
Met
1

gac tcg gcc ctc agc gat ccg cat aac ggc agt gcc gag gca ggc ggc 167
Asp Ser Ala Leu Ser Asp Pro His Asn Gly Ser Ala Glu Ala Gly Gly
5 10 15

ccc acc aac agc act acg cgg ccg cct tcc acg ccc gag ggc atc gcg 215
Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile Ala
20 25 30

ctg gcc tac ggc agc ctc ctg ctc atg gcg ctg ctg ccc atc ttc ttc 263
Leu Ala Tyr Gly Ser Leu Leu Met Ala Leu Leu Pro Ile Phe Phe
35 40 45

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ggc gcc ctg cgc tcc gta cgc tgc gcc cgc ggc aag aat gct tca gac	311
Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser Asp	
50 55 60 65	
atg cct gaa aca atc acc agc cgg gat gcc gcc cgc ttc ccc atc atc	359
Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile Ile	
70 75 80	
gcc agc tgc aca ctc ttg ggg ctc tac ctc ttt ttc aaa ata ttc tcc	407
Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe Ser	
85 90 95	
cag gag tac atc aac ctc ctg ctg tcc atg tat ttc ttc gtg ctg gga	455
Gln Glu Tyr Ile Asn Leu Leu Leu Ser Met Tyr Phe Phe Val Leu Gly	
100 105 110	
atc ctg gcc ctg tcc cac acc atc agc ccc ttc atg aat aag ttt ttt	503
Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe Phe	
115 120 125	
cca gcc agc ttt cca aat cga cag tac cag ctg ctc ttc aca cag ggt	551
Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln Gly	
130 135 140 145	
tct ggg gaa aac aag gaa gag atc atc aat tat gaa ttt gac acc aag	599
Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr Lys	
150 155 160	
gac ctg gtg tgc ctg ggc ctg agc agc atc gtt ggc gtc tgg tac ctg	647
Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr Leu	
165 170 175	
ctg agg aag gta ttt ggc acc aat gtg atg gtg aca gtg gcc aag tcc	695
Leu Arg Lys Val Phe Gly Thr Asn Val Met Val Thr Val Ala Lys Ser	
180 185 190	
ttc gag gca cca ata aaa ttg gtg ttt ccc cag gat ctg ctg gag aaa	743
Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln Asp Leu Leu Glu Lys	
195 200 205	
ggc ctc gaa gca aac aac ttt gcc atg ctg gga ctt gga gat gtc gtc	791
Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly Leu Gly Asp Val Val	
210 215 220 225	
att cca ggg atc ttc att gcc ttg ctg ctg cgc ttt gac atc agc ttg	839
Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser Leu	
230 235 240	
aag aag aat acc cac acc tac ttc tac acc agc ttt gca gcc tac atc	887
Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr Ile	
245 250 255	
ttc ggc ctg ggc ctt acc atc ttc atc atg cac atc ttc aag cat gct	935
Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His Ile Phe Lys His Ala	
260 265 270	

cag cct gcc ctc cta tac ctg gtc ccc gcc tgc atc ggt ttt cct gtc 983
 Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro Val
 275 280 285

ctg gtg gcg ctg gcc aag gga gaa gtg aca gag atg ttc agt tat gag 1031
 Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu Met Phe Ser Tyr Glu
 290 295 300 305

gag tca aat cct aag gat cca gcg gca gtg aca gaa tcc aaa gag gga 1079
 Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr Glu Ser Lys Glu Gly
 310 315 320

aca gag gca tca gca tcg aag ggg ctg gag aag aaa gag aaa 1121
 Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys Lys Glu Lys
 325 330 335

tgatgcggct ggtgcccag cctctcaggg ccagaccaga cagatggggg ctgggcccac 1181

acaggcgtgc accggtagag ggcacaggag gccaaaggga gctccaggac agggcagggg 1241

gcagcaggat acctccagcc aggcctctgt ggcctctgtt tccttctccc tttcttgccc 1301

ctcctctgct cctccccaca ccctgcaggc aaaagaaacc cccagcttcc cccctccccg 1361

ggagccagggt gggaaaagtg ggtgtgattt ttagattttg tattgtggac tgattttgcc 1421

tcacattaaa aactcatccc atggccaggg cgggccactg tgctcctgaa aaaaaaaaaa 1481

aaaaa 1486

<210> 11
 <211> 335
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Clone OA004b derived from T98G cell

<400> 11

Met Asp Ser Ala Leu Ser Asp Pro His Asn Gly Ser Ala Glu Ala Gly
 1 5 10 15

Gly Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile
 20 25 30

Ala Leu Ala Tyr Gly Ser Leu Leu Leu Met Ala Leu Leu Pro Ile Phe
 35 40 45

Phe Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser
 50 55 60

Asp Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile
 65 70 75 80

Ile Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe
 85 90 95

Ser Gln Glu Tyr Ile Asn Leu Leu Leu Ser Met Tyr Phe Phe Val Leu
 100 105 110

Gly Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe
 115 120 125

Phe Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln
 130 135 140

Gly Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr
 145 150 155 160

Lys Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr
 165 170 175

Leu Leu Arg Lys Val Phe Gly Thr Asn Val Met Val Thr Val Ala Lys
 180 185 190

Ser Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln Asp Leu Leu Glu
 195 200 205

Lys Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly Leu Gly Asp Val
 210 215 220

Val Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser
 225 230 235 240

Leu Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr
 245 250 255

Ile Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His Ile Phe Lys His
 260 265 270

Ala Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro
 275 280 285

Val Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu Met Phe Ser Tyr
 290 295 300

Glu Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr Glu Ser Lys Glu
 305 310 315 320

Gly Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys Lys Glu Lys
 325 330 335

<210> 12
 <211> 1080
 <212> DNA
 <213> Homo sapiens

<400> 12
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 agtcaactag tgaattcaaa caacttgaag ctcaatttct ggaaatctcc ctctctcttc 180
 aatcggcctg tggatgtcct ggtcccatct gtcagtctgc aggcatttaa atccttctctg 240
 agatcccagg gcttagagta cgcagtgaca attgaggacc tgcaggccct tttagacaat 300
 gaagatgatg aaatgcaaca caatgaaggg caagaacgga gcagtaataa cttcaactac 360
 ggggcttacc attccctgga agctatttac cacgagatgg acaacattgc cgcagacttt 420
 cctgacctgg cgaggagggt gaagattgga cattcgtttg aaaaccggcc gatgtatgta 480
 ctgaagttca gcaactgggaa aggcgtgagg cggccggccg tttggctgaa tgcaggcatc 540
 cattcccgag agtggatctc ccaggccact gcaatctgga cggcaaggaa gattgtatct 600
 gattaccaga gggatccagc tatcacctcc atcttggaga aaatggatat tttcttggtg 660
 cctgtggcca atcctgatgg atatgtgtat actcaaactc aaaaccgatt atggaggaag 720
 acgcggtccc gaaatcctgg aagctcctgc attggtgctg acccaaatag aagctggaac 780
 gctagttttg caggaaaggg agccagcgac aacccttgct ccgaagtgta ccatggaccc 840
 cacgccaatt cggaagtgga ggtgaaatca gtggtagatt tcatccaaaa acatgggaat 900
 ttcaagtgct tcatcgacct gcacagctac tcgcagctgc tgatgtatcc atatgggtac 960

tcagtcaaaa aggccccaga tgccgaggaa ctgcacaagg tggcgaggct tgcggccaaa 1020
gctctgggctt ctgtgtcggg cactgagtac caagtgggtc ccacctgcac cactgtctta 1080

<210> 13
<211> 3156
<212> DNA
<213> Homo sapiens

<220>
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<223> Clone OAF075b derived from human bone marrow stroma cell HAS303

<220>
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<222> (11)..(1090)

<220>
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<222> (11)..(58)

<220>
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<222> (59)..()

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Met Arg Trp Ile Leu Phe Ile Gly Ala Leu Ile Gly Ser
-15 -10 -5

agc atc tgt ggc caa gaa aaa ttt ttt ggg gac caa gtt ttt agg att 97
Ser Ile Cys Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Phe Arg Ile
-1 1 5 10

aat gtc aga aat gga gac gag atc agc aaa ttg agt caa cta gtg aat 145
Asn Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
15 20 25

tca aac aac ttg aag ctc aat ttc tgg aaa tct ccc tcc tcc ttc aat 193
Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe Asn
30 35 40 45

cgg cct gtg gat gtc ctg gtc cca tct gtc agt ctg cag gca ttt aaa 241
Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala Phe Lys
50 55 60

tcc ttc ctg aga tcc cag ggc tta gag tac gca gtg aca att gag gac 289
Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr Ile Glu Asp
65 70 75

ctg cag gcc ctt tta gac aat gaa gat gat gaa atg caa cac aat gaa 337
Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met Gln His Asn Glu
80 85 90

ggg caa gaa cgg agc agt aat aac ttc aac tac ggg gct tac cat tcc Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr Gly Ala Tyr His Ser 95 100 105	385
ctg gaa gct att tac cac gag atg gac aac att gcc gca gac ttt cct Leu Glu Ala Ile Tyr His Glu Met Asp Asn Ile Ala Ala Asp Phe Pro 110 115 120 125	433
gac ctg gcg agg agg gtg aag att gga cat tcg ttt gaa aac cgg ccg Asp Leu Ala Arg Arg Val Lys Ile Gly His Ser Phe Glu Asn Arg Pro 130 135 140	481
atg tat gta ctg aag ttc agc act ggg aaa ggc gtg agg cgg ccg gcc Met Tyr Val Leu Lys Phe Ser Thr Gly Lys Gly Val Arg Arg Pro Ala 145 150 155	529
gtt tgg ctg aat gca ggc atc cat tcc cga gag tgg atc tcc cag gcc Val Trp Leu Asn Ala Gly Ile His Ser Arg Glu Trp Ile Ser Gln Ala 160 165 170	577
act gca atc tgg acg gca agg aag att gta tct gat tac cag agg gat Thr Ala Ile Trp Thr Ala Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp 175 180 185	625
cca gct atc acc tcc atc ttg gag aaa atg gat att ttc ttg ttg cct Pro Ala Ile Thr Ser Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro 190 195 200 205	673
gtg gcc aat cct gat gga tat gtg tat act caa act caa aac cga tta Val Ala Asn Pro Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu 210 215 220	721
tgg agg aag acg cgg tcc cga aat cct gga agc tcc tgc att ggt gct Trp Arg Lys Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala 225 230 235	769
gac cca aat aga agc tgg aac gct agt ttt gca gga aag gga gcc agc Asp Pro Asn Arg Ser Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser 240 245 250	817
gac aac cct tgc tcc gaa gtg tac cat gga ccc cac gcc aat tcg gaa Asp Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu 255 260 265	865
gtg gag gtg aaa tca gtg gta gat ttc atc caa aaa cat ggg aat ttc Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn Phe 270 275 280 285	913
aag tgc ttc atc gac ctg cac agc tac tcg cag ctg ctg atg tat cca Lys Cys Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met Tyr Pro 290 295 300	961
tat ggg tac tca gtc aaa aag gcc cca gat gcc gag gaa ctc gac aag Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu Leu Asp Lys	1009

305	310	315	
gtg gcg agg ctt gcg gcc aaa gct ctg gct tct	gtg tcg ggc act gag	1057	
Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser	Val Ser Gly Thr Glu		
320	325 330		
tac caa gtg ggt ccc acc tgc acc act gtc tta	taaactgccca aaactgggag	1110	
Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Leu			
335	340		
atactcatca gattgctcca acagaagagg aggaaggctc	tcccgagggc tgtccaggag	1170	
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ctctatccaa cgccataggt tatgggtgtgt gctacataca	cagtcgacgt ttgtcctttc	1650	
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cagcctctag caacccttcc cctcctctct cactgattct	gctccaggaa gggcttggaa	2010	
acaagttctt tgggttcctc tgacttgtgg ataacacagt	ttcatgtact ttttgtagtt	2070	
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aaggttcatt gaaaaatcaa ctgaccaaag gcagatcgat	aggagaaaag gcatacaaaa	2310	
ttttatttta gtgtgcatgg cacaggggaa tcacaggaga	atgatttccc aataacccaa	2370	
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gagggtgggag gcagatatta caggaagggt agggggcgag	ctgtacagga acaaagcttg	2490	

tcttattaag cagataaaagt cctccaggca atctcttgga gctgctctca gaagaataga 2550
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gagggccctc agcatgtcaa aacatcagcc tttgggatat cactttctga gcccaccc 2850
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acacaatgca gcactacgga gcccttaa atgaatgagga gatctatgtg cgctaaaagg 2970
gaatactcac caattgttaa ttgaaaaata catgtgcaga acagcgtaa tagtgtgttc 3030
ccattttttg ttgttggtat tgtttttaaa gagtaggtag actttcagca gggacccaaa 3090
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aaaaaa 3156

<210> 14

<211> 360

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Clone OAF075b derived from human bone marrow stroma cell HAS303

<400> 14

Met Arg Trp Ile Leu Phe Ile Gly Ala Leu Ile Gly Ser Ser Ile Cys
-15 -10 -5 -1

Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Phe Arg Ile Asn Val Arg
1 5 10 15

Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn Ser Asn Asn
20 25 30

Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe Asn Arg Pro Val
35 40 45

Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala Phe Lys Ser Phe Leu
50 55 60

Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr Ile Glu Asp Leu Gln Ala
65 70 75 80

Leu Leu Asp Asn Glu Asp Asp Glu Met Gln His Asn Glu Gly Gln Glu
85 90 95

Arg Ser Ser Asn Asn Phe Asn Tyr Gly Ala Tyr His Ser Leu Glu Ala
100 105 110

Ile Tyr His Glu Met Asp Asn Ile Ala Ala Asp Phe Pro Asp Leu Ala
115 120 125

Arg Arg Val Lys Ile Gly His Ser Phe Glu Asn Arg Pro Met Tyr Val
130 135 140

Leu Lys Phe Ser Thr Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu
145 150 155 160

Asn Ala Gly Ile His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile
165 170 175

Trp Thr Ala Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile
180 185 190

Thr Ser Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn
195 200 205

Pro Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys
210 215 220

Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro Asn
225 230 235 240

Arg Ser Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp Asn Pro
245 250 255

Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu Val Glu Val
260 265 270

Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn Phe Lys Cys Phe

275

280

285

Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met Tyr Pro Tyr Gly Tyr
 290 295 300

Ser Val Lys Lys Ala Pro Asp Ala Glu Glu Leu Asp Lys Val Ala Arg
 305 310 315 320

Leu Ala Ala Lys Ala Leu Ala Ser Val Ser Gly Thr Glu Tyr Gln Val
 325 330 335

Gly Pro Thr Cys Thr Thr Val Leu
 340

<210> 15
 <211> 35
 <212> DNA
 <213> Artificial

<220>
 <223> Primer

<220>
 <221> misc_feature
 <223> n can be any nucleotide

<400> 15
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35

<210> 16
 <211> 27
 <212> DNA
 <213> Artificial

<220>
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 gtccttcagc aaaacagtgg atttaaa

27

<210> 17
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 <212> DNA
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<220>
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<400> 17
ccagaaagca cagccctgat tctgcgt 27

<210> 18
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Primer OA004-F1

<220>
<221> modified_base
<222> (1)..(1)
<223> biotin conjugated base

<400> 18
atgcacatct tcaagcatgc tcag 24

<210> 19
<211> 27
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